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<b>(54) Title:</b> PNEUMOLYSIN MUTANTS AND PNEUMOCOCCAL VACCINES MADE THEREFROM  <b>(57) Abstract</b>  Mutants of pneumolysin that are non-toxic by reason of amino acid substitutions have been constructed. These mutants elicit an immune response in animals that is reactive to wild-type pneumolysin. The invention also encompasses vaccines for humans based on these mutants, including vaccines comprising conjugates with pneumococcal capsular polysaccharides.		

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PNEUMOLYSIN MUTANTS AND PNEUMOCOCCAL VACCINES  
MADE THEREFROM

5 This invention relates to mutants of the toxin pneumolysin and pneumococcal vaccines based on these mutants.

BACKGROUND

10 *Streptococcus pneumoniae* (pneumococcus) is an important pathogen, causing invasive diseases such as pneumonia, meningitis and bacteraemia. Even in regions where effective antibiotic therapy is freely available, the mortality rate from pneumococcal pneumonia can be as high as 19% in hospitalized patients and this increases to 30-40% in patients with bacteraemia. These high mortality rates have been reported in the U.S.A. where pneumonia, of which *S. pneumoniae* is  
15 the commonest cause, is the fifth ranking cause of death. Indeed, pneumonia is the only infectious disease amongst the top ten causes of death in that country. In the United States mortality rates for pneumococcal meningitis range from 13-45%. In developing countries, in excess of 3 million children under the age of 5 years die each year  
20 from pneumonia, and again *S. pneumoniae* is the commonest causative agent. *S. pneumoniae* also causes less serious, but highly prevalent infections such as otitis media and sinusitis, which have a significant impact on health-care costs in developed countries. Otitis media is especially important in young children; sinusitis affects both  
25 children and adults.

In the late 1970's, a vaccine was licensed for the purpose of preventing serious infections, especially bacterial pneumonia and for protecting certain groups, such as splenectomized individuals and young children,  
30 who are particularly susceptible to fulminating pneumococcal disease. The vaccine is composed of purified capsular polysaccharides, which are the predominant pneumococcal surface antigens. However, each serotype of *S. pneumoniae* (of which there are 83) has a structurally distinct capsular polysaccharide, and immunization with one serotype  
35 confers no protection whatsoever against the vast majority of the others. The vaccine currently licensed in Australia contains polysaccharides purified from the 23 most common serotypes, which account for approximately 90% of pneumococcal infections in this country.

Protection even against those serotypes contained in the vaccine is by no means complete, and there have been several reports of serious, even fatal infections occurring in vaccinated high-risk individuals. The efficacy of the vaccine is poorest in young children, and several studies, including one conducted in Adelaide, have shown that the existing formulation has little or no demonstrable clinical benefit in this group. This apparent failure of the vaccine appears to be related to the poor immunogenicity of certain pneumococcal polysaccharides in children under 5 years of age. We have shown that the antibody response is particularly poor to the five serotypes which most commonly cause disease in children (types 6, 14, 18, 19 and 23). Indeed, the antibody response to these pneumococcal polysaccharides only approaches adult levels in children over 8 years of age at the time of vaccination.

In view of this, a vaccine, including antigens other than the capsular polysaccharides seems to be required to protect young children from pneumococcal infection. One such antigen could be pneumolysin, a protein toxin produced by all virulent *S. pneumoniae* isolates. Immunization of mice with this protein has been found to confer a degree of protection from pneumococcal infection.

However there is a difficulty in that pneumolysin is toxic to humans. Thus pneumolysin included in a vaccine must therefore be substantially non-toxic. However, the rendering of a pneumolysin non-toxic by most currently employed methods would be likely to alter the basic configuration of the protein so as to be immunogenically distinct from the native or wild-type pneumolysin. An immune response elicited by an altered protein that is immunogenically distinct from the native pneumolysin will have a decreased protective capacity or no protective capacity. Thus the difficulty is to produce an altered pneumolysin that is non-toxic and at the same time sufficiently immunogenically similar to the toxic form to elicit a protective immune response.

An altered pneumolysin with the above characteristics can then be used in a number of ways in a vaccine. Thus the altered pneumolysin may be used by itself to immunise, or alternatively the altered pneumolysin may be conjugated to pneumococcal polysaccharide, or

alternatively may be included in a vaccine wherein pneumococcal polysaccharides may be conjugated to another protein and the altered pneumolysin is present in a non-conjugated form only. Alternatively, pneumococcal polysaccharide and pneumolysin may both be used in  
5 an unconjugated form.

#### DESCRIPTION OF INVENTION

In a broad form therefore the invention may be said to reside in an altered pneumolysin being substantially non-toxic and being capable of  
10 eliciting an immune response in an animal being reactive to wild-type pneumolysin.

Preferably the altered pneumolysin has reduced complement binding activity as compared to wild-type pneumolysin. Reduction in the  
15 complement binding activity results in less inflammation at the site of administering the vaccine.

Preferably the altered pneumolysin has reduced Fc binding activity as compared to wild-type pneumolysin. Reduction in the Fc binding  
20 activity results in less inflammation at the site of administering the vaccine.

Preferably the altered pneumolysin is altered by reason of one or more amino acid substitutions relative to wild-type pneumolysin.  
25

The pneumolysin may be altered in that the amino acid present at any one or more than one of residue sites 367, 384, 385, 428, 433 or 435 of wild-type pneumolysin are replaced, removed or blocked.

30 In a further form the invention could be said to reside in a vaccine including an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.

35 Preferably the vaccine comprises capsular polysaccharide material conjugated with the altered pneumolysin.

The capsular material may be derived from any one or more of the *Streptococcus pneumoniae* serotypes 6A, 6B, 14, 18C, 19A, 19F, 23F, 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F.

- 5 In this embodiment serotypes which are commonly associated with disease in children, and to which children generally have a poor immune response, may be specifically targeted (i.e. Danish serotypes 6A, 6B, 14, 18C, 19A, 19F and 23F). Other common serotypes contained in the present 23-valent Merck Sharp and Dohme vaccine  
10 (Pneumovax 23) however, could also be used to synthesize conjugates (i.e. types 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F) or indeed any other serotype. Conjugation of any pneumococcal polysaccharides to the protein carrier ensures good T-cell dependent immunogenicity in children, such that protective levels  
15 of anti-polysaccharide antibody are produced.

The combination of the altered pneumolysin together with the capsular material will ensure an extra degree of protection, particularly against serotypes of *S. pneumoniae* whose polysaccharides are not  
20 incorporated in the existing vaccine formulations.

The vaccine is preferably administered by sub-cutaneous injection, with or without an approved adjuvant, such as alumina gel.

- 25 In another form the invention could be said to reside in a recombinant clone including a replicon and a DNA sequence encoding an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.

30 In yet another form the invention could be said to reside in a method of producing an altered pneumolysin including the steps of purifying said altered pneumolysin from an expression system including a recombinant clone with DNA encoding an altered pneumolysin said  
35 pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal reactive to wild-type pneumolysin.

Preferrably the expression system is a culture of a host cell including a recombinant clone with DNA encoding the altered pneumolysin.

5 In another form the invention could be said to reside in a method of producing a vaccine including the step of amplifying a recombinant clone encoding an altered pneumolysin, inducing transcription and translation of said cloned material, the purification of altered pneumolysin, and the step of conjugating the altered pneumolysin with a capsular polysaccharide, the altered pneumolysin having  
10 substantially reduced toxic activity as compared with wild-type pneumolysin.

For a better understanding of the invention specific embodiments of the  
15 invention will now be described with reference to diagrams wherein:-

FIG. 1 Is the DNA sequence of the gene encoding wild-type pneumolysin,

20 FIG. 2 Is the DNA sequence of an altered gene encoding wild type pneumolysin used for cloning the pneumolysin gene into an expression vector,

FIG. 3 Is the amino acid sequence of the wild-type pneumolysin as  
25 derived from the DNA sequence of the gene encoding the wild type pneumolysin, and

FIG. 4 shows the amino acid sequence of pneumolysin showing amino acid substitutions introduced by site directed mutagenesis.  
30

Recombinant DNA techniques have been used to construct non-toxic pneumolysin derivatives suitable for administration to humans. To achieve this, the *S. pneumoniae* gene encoding pneumolysin was  
35 cloned into *Escherichia coli* and its complete DNA sequence determined. The DNA sequence is shown in Figure 1 and the derived amino acid sequence is shown in Figure 3.

Three regions of the pneumolysin gene were subjected to oligonucleotide-directed mutagenesis. The first region encodes amino acids 427 - 437 in the protein sequence, and is indicated by an underline in Figure 3. This 11 amino acid sequence shows absolute  
5 homology with similar regions in other related thiol activated toxins thus is thought to be responsible for the haemolytic activity and hence toxic activity of the toxin. The other two regions encode amino acids 257 - 297 and amino acids 368 - 397 and are also indicated by an underline in Figure 3. These two regions of the toxin have substantial  
10 amino acid sequence homology with human C-reactive protein (CRP), and by inference therefore, are thought to be responsible for the ability of pneumolysin to bind the Fc region of immunoglobulins and to activate complement. Fifteen separate mutations in the pneumolysin gene, resulting in single amino acid substitutions, were constructed, as  
15 shown in Figure 4. In an effort to maintain the structure of the altered pneumolysin, conservative substitutions were made, so that amino acids are substituted with amino acids of a similar nature.

For the region involved in haemolytic activity, Cys 428 -> Gly, Cys 428 -> Ser, Trp<sub>433</sub> -> Phe, Glu<sub>434</sub> -> Asp and Trp<sub>435</sub> -> Phe each reduced  
20 haemolytic activity by 97%, 90%, 99%, 75% and 90% respectively. The other mutations in that region (Cys<sub>428</sub> -> Ala, Glu<sub>434</sub> -> Gln and Trp<sub>436</sub> -> Phe) did not affect haemolytic activity. Mutating a separate region of the toxin thought to be responsible for binding to target cell membranes  
25 also affects haemolytic activity of the protein. This substitution, His<sub>367</sub> -> Arg, completely inhibits haemolytic activity. This is a quite unpredictable finding in that His<sub>367</sub> -> Arg therefore shows a greater inhibition of this property than the substitutions made within the 11 amino acid region thought to be responsible for haemolytic activity.

30 Mutations in the CRP-like domains were tested for ability to activate complement. For Trp<sub>379</sub> -> Phe, Tyr<sub>384</sub> -> Phe, Asp<sub>385</sub> -> Asn, and Trp<sub>397</sub> -> Phe, complement activation was reduced by 20%, 70%, 100% and 15%, respectively. The other mutations in the CRP-like  
35 domains shown in Figure 4 do not reduce complement activation.



Importantly, the above mutations which affect either haemolytic activity or complement activation do not impair the immunogenicity of the proteins, compared with native or wild-type pneumolysin.

- 5 Thus although His<sub>367</sub> -> Arg is the preferred mutation to reduce the haemolytic activity, a combination of two or more mutants effecting reduced haemolytic activity can also achieve a very high level of reduction in haemolytic activity. Similarly Asp<sub>385</sub> -> Asn is the preferred mutation to achieve reduced complement activation, however a  
10 combination of two or more other mutants that reduce the activity to a lesser degree can also be used.

In a preferred embodiment the pneumolysin derivative for use in the vaccine would contain a combination of certain of the above mutations  
15 such that the protein is unable to activate complement in addition to having zero haemolytic activity. Examples of such combination are:-

- 1) His<sub>367</sub> -> Arg + Asp<sub>385</sub> -> Asn,
- 2) His<sub>367</sub> -> Arg + Asp<sub>385</sub> -> Asn + either Cys<sub>428</sub> -> Gly or Trp<sub>433</sub> -> Phe
- 20 3) Asp<sub>385</sub> -> Asn + Cys<sub>428</sub> -> Gly + Trp<sub>433</sub> -> Phe

These then are some preferred combinations, however it is to be understood that other combinations of mutations can be used to make up the altered pneumolysin for use in a vaccine. Further the altered  
25 pneumolysin may comprise any one of the individual mutations with sufficiently reduced activity.

High level expression of the altered pneumolysin from DNA encoding the altered pneumolysin can be achieved by using any one of a number  
30 of conventional techniques including the expression in a prokaryotic host with the DNA cloned appropriately within any one of the many expression vectors currently available, or cloned appropriately within the host chromosome; expression in a eukaryotic host with the DNA cloned appropriately either within an expression vector or cloned within  
35 the host chromosome; or within an *in vitro* expression system such as may comprise purified components necessary for expression of altered pneumolysin.

To achieve high level expression of the mutated pneumolysin gene, it has been cloned into the vector pKK233-2 for expression within *Escherichia coli* or other like prokaryote. This vector included ampicillin and tetracycline resistance genes, the *trc* promoter (which can be regulated by IPTG [isopropyl- $\beta$ -D-thiogalactopyranoside]), and a *lac Z* ribosome binding site adjacent to an ATG initiation codon incorporating an *NcoI* restriction site. Immediately downstream from the initiation codon there are restriction sites for *PstI* and *HindIII*, followed by a strong T<sub>1</sub> T<sub>2</sub> transcription terminator. Prior to insertion into pKK233-2, a *NcoI* restriction site was constructed at the 5' end of the pneumolysin coding sequence (at the initiation codon) by oligonucleotide-directed mutagenesis, as shown in Figure 2. This enabled the proximal end of the altered pneumolysin gene to be cloned into the *NcoI* site of pKK233-2; a *HindIII* site approximately 80 bases downstream from the pneumolysin termination codon was used to splice the distal end of the altered gene into the compatible site in pKK233-2. The mutant pneumolysin derivative could however, be cloned into any one of a number of high expression vector systems.

The mutant pneumolysin is prepared as follows: *E. coli* cells harbouring the above recombinant plasmid are first grown in 9 litre cultures in Luria Bertani (or any other appropriate) medium, supplemented with the appropriate antibiotic, at 37° C, with aeration. When the culture reaches the late logarithmic phase of growth, IPTG is added to a final concentration of 20 $\mu$ M (to induce expression of the altered pneumolysin gene) and incubation is continued for a further 2 to 3 hours.

Cells are then harvested by centrifugation or ultrafiltration and lysed by treatment with EDTA and lysozyme, followed by sonication, or by disruption in a French pressure cell. Cell debris is removed by centrifugation and the extract is then dialysed extensively against 10mM sodium phosphate (pH7.0). The material is then loaded onto a column of DEAE-cellulose and eluted with a linear gradient of 10-250mM sodium phosphate (pH7.0). Fractions containing peak levels of the pneumolysin derivative are pooled, concentrated by ultrafiltration and loaded onto a column of Sephacryl S-200. This column is developed in 50mM sodium phosphate (pH7.0) and again fractions with high levels of pneumolysin derivative are pooled, concentrated by

ultrafiltration and stored in 50% glycerol at -15°C. The final product is greater than 95% pure, as judged by SDS-polyacrylamide gel electrophoresis. Hydrophobic interaction chromatography on Phenyl-Sepharose is an alternative purification which could also be used.

- 5 However it is to be understood that this is only one method of purification of the altered pneumolysin, and other, alternative methods (including High Pressure Liquid Chromatography) may be employed.

- 10 This purified altered pneumolysin can then be administered as a vaccine at appropriate levels, either by itself or in combination with other antigens. In one form the pneumolysin may be conjugated with polysaccharide derived from any one or more of the variety of pneumococcal strains described above.

- 15 The mutant pneumolysin can be conjugated to the various serotypes of polysaccharide by a range of methods. The first involves preparation of an activated polysaccharide by treating pure polysaccharide (available commercially) with cyanogen-bromide and adipicacid dihydrazide (ADH). The ADH-polysaccharide is then combined with the mutant  
20 pneumolysin in the presence of 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide - HCl. Conjugated material is separated from the reactants by chromatography through Sepharose CL-4B.

- Alternatively, the polysaccharide-mutant pneumolysin conjugates can  
25 be prepared using bifunctional reagents such as N-succinimidyl-6(4'-azido-2'-nitrophenylamino)hexanoate (SANPAH). Pure polysaccharide dissolved in phosphate buffered saline, is reacted with SANPAH in the presence of a strong white light source. Unreacted SANPAH is then separated from activated polysaccharide by chromatography on  
30 Sephadex G-50. Activated polysaccharide is then conjugated to the mutant pneumolysin in 0.2M borate buffer (pH8.5). Any excess reactive groups are then blocked with lysine, and the polysaccharide-protein conjugate is separated from the other reactants by chromatography on Sepharose CL-4B. Conjugates could also be prepared by reductive  
35 amination with cyanoborohydride.

Alternatively another protein, such as inactivated tetanus toxin, can be conjugated with the desired polysaccharides and altered pneumolysin can be added to the vaccine in an unconjugated form.

5

This then describes the best method of performing the invention however it is to be understood that the invention is not limited thereto.

1. An altered pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.
- 5 2. An altered pneumolysin as in claim one having reduced complement binding activity as compared to wild-type pneumolysin.
3. An altered pneumolysin as in any one of claims 1 or 2 having reduced Fc binding activity as compared to wild-type pneumolysin.
- 10 4. An altered pneumolysin as in any one of claims 1, 2, or 3 wherein said altered pneumolysin is altered by reason of one or more amino acid substitutions within wild type pneumolysin.

- 15 5. An altered pneumolysin having the following amino acid sequence:-
 

Met	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu	Ala	Met
1										11		
Asn	Tyr	Asp	Lys	Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu
							21					
Ser	Ile	Glu	Asn	Arg	Phe	Ile	Lys	Glu	Gly	Asn	Gln	Leu
				31								
Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys	Lys	Arg	Ser
	41										51	
Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr
								61				
Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val
					71							
Asp	Glu	Thr	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala
		81										91
Val	Asp	Arg	Ala	Pro	Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro
									101			
Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu	Gln	Val	Glu	Asp
						111						
Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	Leu
			121									
Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn
										141		
Val	Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His
							151					
Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe
				161								
Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe	Asn	Ser
	171										181	
Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe
								191				

	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys
						201							
5	Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu
			211										221
	Asp	Leu	Lys	Gln	Arg	Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu
										231			
	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	Arg	Gln	Val	Tyr
							241						
10	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	Glu
				251									
	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala
	261										271		
15	Pro	Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu
								281					
	Val	Lys	Ala	Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly
					291								
	Ala	Arg	Val	Val	Thr	Gly	Lys	Val	Asp	Met	Val	Glu	Asp
	301											311	
20	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	His	Pro
									321				
	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp
						331							
25	Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val
			341										351
	Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu
										361			
	Leu	Asp	R <sub>1</sub>	Ser	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Tyr	Ile
							371						
30	Thr	R <sub>2</sub>	Asp	Glu	Leu	Ser	R <sub>3</sub>	R <sub>4</sub>	His	Gln	Gly	Lys	Glu
				381									
	Val	Leu	Thr	Pro	Lys	Ala	R <sub>5</sub>	Asp	Arg	Asn	Gly	Gln	Asp
	391										401		
35	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly
								411					
	Asn	Val	Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	R <sub>6</sub>	Thr
					421								
	Gly	Leu	Ala	R <sub>7</sub>	R <sub>8</sub>	R <sub>9</sub>	Trp	Arg	Thr	Val	Tyr	Glu	Lys
	431											441	
40	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	Arg	Thr	Ile	Ser	Ile
									451				
	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys	Val
						461							
45	Glu	Asn	Asp										
			471										

wherein R<sub>1</sub> is His or Arg, R<sub>2</sub> is Trp or Phe, R<sub>3</sub> is Tyr or Phe, R<sub>4</sub> is Asp or Asn, R<sub>5</sub> is Trp or Phe, R<sub>6</sub> is Cys, Gly, or Ser, R<sub>7</sub> is Trp or Phe, R<sub>8</sub> is Glu, or Asp, R<sub>9</sub> is Trp or Phe, and wherein at least one of the residues R<sub>1</sub>,

50 R<sub>6</sub>, R<sub>7</sub>, R<sub>8</sub>, or R<sub>9</sub> is other than wild-type.

6. An altered pneumolysin as in claim 5 wherein wherein R<sub>1</sub> is Arg, R<sub>2</sub> is Trp, R<sub>3</sub> is Tyr, R<sub>4</sub> is Asn, R<sub>5</sub> is Trp, R<sub>6</sub> is Cys, R<sub>7</sub> is Trp, R<sub>8</sub> is Glu, and R<sub>9</sub> is Trp.
- 5 7. A vaccine including an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.
8. A vaccine as in claim 7 wherein the altered pneumolysin is as  
10 claimed in any one of claims 2 to 6.
9. A vaccine comprising capsular polysaccharide material conjugated with a protein carrier and non-conjugated protein material, the capsular polysaccharide material being derived from any one or  
15 more than one of the *Streptococcus pneumoniae* serotypes, and the non-conjugated protein material being an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal reactive to wild type pneumolysin.
- 20 10. A vaccine as in claim 9 wherein the capsular material is derived from any one or more of the *Streptococcus pneumoniae* serotypes 6A, 6B, 14, 18C, 19A, 19F, 23F, 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F.
- 25 11. A vaccine as in either claim 9 or 10 wherein the altered pneumolysin is as claimed in as in any one of claims 2 to 6.
12. A vaccine comprising capsular polysaccharide material conjugated with a protein carrier, the capsular polysaccharide material  
30 being derived from any one or more than one of the *Streptococcus pneumoniae* serotypes, and the protein carrier being an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal reactive to wild type pneumolysin.
- 35 13. A vaccine as in claim 12 wherein the capsular material is derived from any one or more of the *Streptococcus pneumoniae* serotypes 6A,

6B, 14, 18C, 19A, 19F, 23F, 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F.

14. A vaccine as in either claim 12 or 13 wherein the altered  
5 pneumolysin is as claimed in any one of claims 2 to 6.

15. A recombinant plasmid including a DNA sequence encoding an  
altered pneumolysin as claimed in any one of claims 1 to 6.

10 16. A hybrid host cell including a recombinant plasmid as claimed in  
claim 9 said recombinant plasmid including an inducible expression  
control operable for expression of said altered pneumolysin encoding  
DNA within a host cell.

15 17. A method of producing an altered pneumolysin including the  
steps of purifying said altered pneumolysin from an expression system  
including a recombinant plasmid with DNA encoding an altered  
pneumolysin said pneumolysin being substantially non-toxic and being  
capable of eliciting an immune response in an animal reactive to wild  
20 type pneumolysin.

18. A method of producing an altered pneumolysin including the  
steps of purifying said altered pneumolysin from a culture of a host cell  
including a recombinant clone with DNA encoding an altered  
25 pneumolysin said pneumolysin being substantially non-toxic and being  
capable of eliciting an immune response in an animal said immune  
response being reactive to wild type pneumolysin.

19. A method of producing a vaccine including the step of amplifying  
30 a recombinant clone encoding an altered pneumolysin, inducing  
transcription and translation of said cloned material, the purification of  
altered pneumolysin, and the step of conjugating the altered  
pneumolysin with a capsular polysaccharide, the altered pneumolysin  
having substantially reduced toxic activity as compared with wild type  
35 pneumolysin.

20 A method of producing a vaccine as in claim 19 wherein said  
altered pneumolysin is as claimed in any one of claims 2 to 6.



21. An altered pneumolysin as hereinbefore described with reference to the examples.

5 22. A vaccine including an altered pneumolysin as hereinbefore described with reference to the examples.

23. A method of producing a vaccine as hereinbefore described with reference to the examples.

10

AGATGGCAAA TAAAGCAGTA AATGACTTTA TACTAGCTAT GAATTACGAT  
AAAAAGAAAC TCTTGACCCA TCAGGGAGAA AGTATTGAAA ATCGTTTCAT  
CAAAGAGGGT AATCAGCTAC CCGATGAGTT TGTTGTTATC GAAAGAAAGA  
AGCGGAGCTT GTCGACAAAT ACAAGTGATA TTTCTGTAAC AGCTACCAAC  
GACAGTCGCC TCTATCCTGG AGCACTTCTC GTAGTGGATG AGACCTTGTT  
AGAGAATAAT CCCACTCTTC TTGCGGTTGA TCGTGCTCCG ATGACTTATA  
GTATTGATTT GCCTGGTTTG GCAAGTAGCG ATAGCTTTCT CCAAGTGGAA  
GACCCAGCA ATTCAAGTGT TCGCGGAGCG GTAAACGATT TGTTGGCTAA  
GTGGCATCAA GATTATGGTC AGGTCAATAA TGTCCCAGCT AGAATGCAGT  
ATGAAAAAAT AACGGCTCAC AGCATGGAAC AACTCAAGGT CAAGTTTGGT  
TCTGACTTTG AAAAGACAGG GAATTCTCTT GATATTGATT TTA ACTCTGT  
CCATT CAGGT GAAAAGCAGA TTCAGATTGT TAATTTTAAG CAGATTTATT  
ATACAGTCAG CGTAGACGCT GTTAAAAATC CAGGAGATGT GTTTC AAGAT  
ACTGTAACGG TAGAGGATTT AAAACAGAGA GGAATTTCTG CAGAGCGTCC  
TTTGGTCTAT ATTT CGAGTG TTGCTTATGG GCGCCAAGTC TATCTCAAGT  
TGGA AACCAC GAGTAAGAGT GATGAAGTAG AGGCTGCTTT TGAAGCTTTG  
ATAAAAGGAG TCAAGGTAGC TCCTCAGACA GAGTGGAAGC AGATTTTGGGA  
CAATACAGAA GTGAAGGCGG TTATTTTAGG GGGCGACCCA AGTTCGGGTG  
CCCGAGTTGT AACAGGCAAG GTGGATATGG TAGAGGACTT GATTCAAGAA  
GGCAGTCGCT TTACAGCAGA TCATCCAGGC TTGCCGATTT CCTATACAAC  
TTCTTTTTTA CGTGACAATG TAGTTGCGAC CTTTCAAAAC AGTACAGACT  
ATGTTGAGAC TAAGGTTACA GCTTACAGAA ACGGAGATTT ACTGCTGGAT  
CATAGTGGTG CCTATGTTGC CCAATATTAT ATTACTTGGG ATGAATTATC  
CTATGATCAT CAAGGTAAGG AAGTCTTGAC TCCTAAGGCT TGGGACAGAA  
ATGGGCAGGA TTGACGGCT CACTTTACCA CTAGTATTCC TTTAAAAGGG  
AATGTTCGTA ATCTCTCTGT CAAAATTAGA GAGTGTACCG GGCTTGCCTG  
GGAATGGTGG CGTACGGTTT ATGAAAAAAC CGATTTGCCA CTAGTGC GTA  
AGCGGACGAT TTCTATTTGG GGAACA ACTC TCTATCCTCA GG TAGAGGAT  
AAGGTAGAAA ATGAC

FIGURE 1 DNA sequence of pneumolysin gene. ATG start codon underlined

CCATGGCAAA TAAAGCAGTA AATGACTTTA TACTAGCTAT GAATTACGAT  
AAAAAGAAAC TCTTGACCCA TCAGGGAGAA AGTATTGAAA ATCGTTTCAT  
CAAAGAGGGT AATCAGCTAC CCGATGAGTT TGTGTTATC GAAAGAAAGA  
AGCGGAGCTT GTCGACAAAT ACAAGTGATA TTTCTGTAAC AGCTACCAAC  
GACAGTCGCC TCTATCCTGG AGCACTTCTC GTAGTGGATG AGACCTTGTT  
AGAGAATAAT CCCACTCTTC TTGCGGTTGA TCGTGCTCCG ATGACTTATA  
GTATTGATTT GCCTGGTTTG GCAAGTAGCG ATAGCTTTCT CCAAGTGGAA  
GACCCCAGCA ATTCAAGTGT TCGCGGAGCG GTAAACGATT TGTGCGCTAA  
GTGGCATCAA GATTATGGTC AGGTCAATAA TGTCCCAGCT AGAATGCAGT  
ATGAAAAAAT AACGGCTCAC AGCATGGAAC AACTCAAGGT CAAGTTTGGT  
TCTGACTTTG AAAAGACAGG GAATTCTCTT GATATTGATT TTAAGTCTGT  
CCATTCAGGT GAAAAGCAGA TTCAGATTGT TAATTTTAAG CAGATTTATT  
ATACAGTCAG CGTAGACGCT GTTAAAAATC CAGGAGATGT GTTTCAGAT  
ACTGTAACGG TAGAGGATTT AAAACAGAGA GGAATTTCTG CAGAGCGTCC  
TTTGGTCTAT ATTTGAGTG TTGCTTATGG GCGCCAAGTC TATCTCAAGT  
TGGAACCAC GAGTAAGAGT GATGAAGTAG AGGCTGCTTT TGAAGCTTTG  
ATAAAGGAG TCAAGGTAGC TCCTCAGACA GAGTGGAAGC AGATTTTGGA  
CAATACAGAA GTGAAGGCGG TTATTTTAGG GGGCGACCCA AGTTCGGGTG  
CCCGAGTTGT AACAGGCAAG GTGGATATGG TAGAGGACTT GATTCAAGAA  
GGCAGTCGCT TTACAGCAGA TCATCCAGGC TTGCCGATTT CCTATACAAC  
TTCTTTTTTA CGTGACAATG TAGTTGCGAC CTTTCAAAC AGTACAGACT  
ATGTTGAGAC TAAGGTTACA GCTTACAGAA ACGGAGATTT ACTGCTGGAT  
CATAGTGGTG CCTATGTTGC CCAATATTAT ATTACTTGGG ATGAATTATC  
CTATGATCAT CAAGGTAAGG AAGTCTTGAC TCCTAAGGCT TGGGACAGAA  
ATGGGCAGGA TTTGACGGCT CACTTTACCA CTAGTATTCC TTTAAAAGGG  
AATGTTTCGTA ATCTCTCTGT CAAAATTAGA GAGTGTACCG GGCTTGCCTG  
GGAATGGTGG CGTACGGTTT ATGAAAAAAC CGATTGCCA CTAGTGCGTA  
AGCGGACGAT TTCTATTTGG GGAACAACCTC TCTATCCTCA GGTAGAGGAT  
AAGGTAGAAA ATGAC

FIGURE 2 DNA sequence of modified pneumolysin gene.  
An NcoI restriction site (underlined) has  
been introduced at the start codon

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Met 1	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu 11	Ala	Met
Asn	Tyr	Asp	Lys	Lys	Lys	Leu 21	Leu	Thr	His	Gln	Gly	Glu
Ser	Ile	Glu	Asn	Arg 31	Phe	Ile	Lys	Glu	Gly	Asn	Gln	Leu
Pro 41	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys	Lys	Arg 51	Ser
Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser 61	Val	Thr	Ala	Thr
Asn	Asp	Ser	Arg	Leu	Tyr 71	Pro	Gly	Ala	Leu	Leu	Val	Val
Asp	Glu	Thr 81	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala 91
Val	Asp	Arg	Ala	Pro	Met	Thr	Tyr	Ser	Ile 101	Asp	Leu	Pro
Gly	Leu	Ala	Ser	Ser	Asp	Ser 111	Phe	Leu	Gln	Val	Glu	Asp
Pro	Ser	Asn	Ser 121	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	Leu
Leu 131	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val 141	Asn	Asn
Val	Pro	Ala	Arg	Met	Gln	Tyr	Glu 151	Lys	Ile	Thr	Ala	His
Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe
Glu 171	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe	Asn 181	Ser
Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln 191	Ile	Val	Asn	Phe
Lys	Gln	Ile	Tyr	Tyr	Thr 201	Val	Ser	Val	Asp	Ala	Val	Lys
Asn	Pro	Gly 211	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu 221

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Asp Leu Lys Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu  
 231

Val Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr  
 241

Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu Val Glu  
 251

Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala  
 261 271

Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu  
 281

Val Lys Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly  
 291

Ala Arg Val Val Thr Gly Lys Val Asp Met Val Glu Asp  
 301 311

Leu Ile Gln Glu Gly Ser Arg Phe Thr Ala Asp His Pro  
 321

Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg Asp  
 331

Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val  
 341 351

Glu Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu  
 361

Leu Asp His Ser Gly Ala Tyr Val Ala Gln Tyr Tyr Ile  
 371

Thr Trp Asp Glu Leu Ser Tyr Asp His Gln Gly Lys Glu  
 381

Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly Gln Asp  
 391 401

Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly  
 411

Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr  
 421

Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys  
 431 441

Thr Asp Leu Pro Leu Val Arg Lys Arg Thr Ile Ser Ile  
 451

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Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp Lys Val  
461

Glu Asn Asp  
471

**Figure 3**

Met	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu	Ala	Met
1										11		
Asn	Tyr	Asp	Lys	Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu
						21						
Ser	Ile	Glu	Asn	Arg	Phe	Ile	Lys	Glu	Gly	Asn	Gln	Leu
			31									
Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys	Lys	Arg	Ser
	41										51	
Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr
								61				
Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val
					71							
Asp	Glu	Thr	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala
		81										91
Val	Asp	Arg	Ala	Pro	Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro
									101			
Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu	Gln	Val	Glu	Asp
						111						
Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	Leu
			121									
Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn
131										141		
Val	Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His
							151					
Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe
				161								
Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe	Asn	Ser
	171										181	
Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe
								191				
Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys
					201							
Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu
		211										221
Asp	Leu	Lys	Gln	Arg	Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu
									231			

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Val	Tyr	Ile	Ser	Ser	Val	Ala 241	Tyr	Gly	Arg	Gln	Val	Tyr		
Leu	Lys	Leu	Glu 251	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	Glu		
		Trp 												
Ala 261	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys 271	Val	Ala		
				Phe 										
Pro	Gln	Thr	Glu	Trp	Lys	Gln	Ile 281	Leu	Asp	Asn	Thr	Glu		
Val	Lys	Ala	Val	Ile 291	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly		
Ala	Arg 301	Val	Val	Thr	Gly	Lys	Val	Asp	Met	Val	Glu 311	Asp		
Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr 321	Ala	Asp	His	Pro		
Gly	Leu	Pro	Ile	Ser	Tyr 331	Thr	Thr	Ser	Phe	Leu	Arg	Asp		
Asn	Val	Val 341	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val 351		
Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn	Gly 361	Asp	Leu	Leu		
		Arg 												
Leu	Asp	His	Ser	Gly	Ala	Tyr 371	Val	Ala	Gln	Tyr	Tyr	Ile		
		Phe 												
Thr	Trp	Asp	Glu 381	Leu	Ser	Tyr	Phe 	Asn 	Asp	His	Gln	Gly	Lys	Glu
							Phe 							
Val 391	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly 401	Gln	Asp		
Leu	Thr	Ala	His	Phe	Thr	Thr	Ser 411	Ile	Pro	Leu	Lys	Gly		



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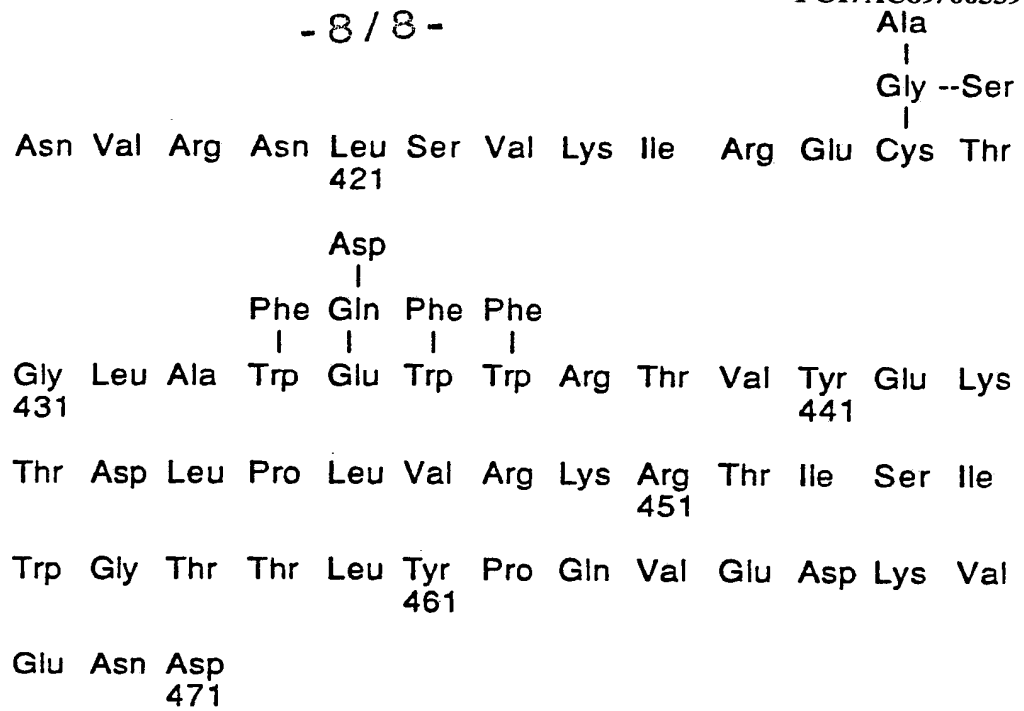


Figure 4

## INTERNATIONAL SEARCH REPORT

International Application No. PCT/AU 89/00539

## I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) 6

According to International Patent Classification (IPC) or to both National Classification and IPC  
 Int.Cl.<sup>5</sup> C07K 13/00, C12P 21/00, C12N 15/31, C07H 21/04

## II. FIELDS SEARCHED

Minimum Documentation Searched 7

Classification System	Classification Symbols
IPC	Derwent databases: WPI, WPIL, USPA: keywords STREPTOCOCCUS PNEUMONIAE, PNEUMOCOCCUS, PNEUMOLYSIN HAEMOLYSIN, HEMOLYSIN, CBR, COMPLEMENT BINDING REGION CPR, REACTIVE PROTEIN

Documentation Searched other than Minimum Documentation  
 to the Extent that such Documents are Included in the Fields Searched 8

Aust Class: C07K 13/00, 15/04  
 C12N 15/31 CHEM ABS using keywords above

## III. DOCUMENTS CONSIDERED TO BE RELEVANT 9

Category*	Citation of Document, with indication, where appropriate, of the relevant passages 12	Relevant to Claim No 13
PX	Infection and Immunity, Vol 57 (8) Aug 1989 p2547-2552 F.K. SAUNDERS et al "Pneumolysin, the Thiol-Activated Toxin of <u>Streptococcus pneumoniae</u> , does not require a Thiol Group for In Vitro Activity"	1, 4-5, 15-21
A	Infection and Immunity, Vol 55 (5) May 1987, p1184-1189 WALKER, J.A. et al "Molecular Cloning, Characterization, and complete Nucleotide Sequence of the Gene for Pneumolysin, the Sulfhydryl-Activated Toxin of <u>Streptococcus pneumoniae</u>	1-22
A	Journal of Clinical Microbiology Feb 1987 p222-225 Krzysztof Kancierski et al "Production and Purification of <u>Streptococcus pneumoniae</u> Hemolysin (Pneumolysin)	1-22

\* Special categories of cited documents: 10 "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

## IV. CERTIFICATION

Date of the Actual Completion of the International Search 6 April 1990 (06.04.90)	Date of Mailing of this International Search Report 12 April 1990
International Searching Authority Australian Patent Office	Signature of Authorized Officer R. SAWYER